

S. Prasad

CRF Error Corrected by the STIC Systems Branch

1600-18

Serial Number: 09/714792

CRF Processing Date: 4/10/2002  
Edited by: AN  
Verified by: AN (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:  
\_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:  
\_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:  
\_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:  
\_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:  
\_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically:  
\_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically:  
\_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:  
\_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☒ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: 4
- ☐ Other:  
\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_

RECEIVED

APR 17 2002

TECH CENTER 1600/2900



#18  
 LMS  
 4-30-02



1646

## RAW SEQUENCE LISTING

DATE: 04/10/2002

PATENT APPLICATION: US/09/714,792

TIME: 18:20:44

Input Set : N:\jumbos\714792.txt

Output Set: N:\CRF3\04102002\I714792.raw

## SEQUENCE LISTING

## 4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Collins, Mary  
 7 Donaldson, Debra  
 8 Fitz, Lori  
 9 Neben, Tamlyn  
 10 Whitters, Matthew  
 11 Wood, Clive

13 (ii) TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN

15 (iii) NUMBER OF SEQUENCES: 9

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Genetics Institute, Inc.

19 (B) STREET: 87 CambridgePark Drive

20 (C) CITY: Cambridge

21 (D) STATE: MA

22 (E) COUNTRY: USA

23 (F) ZIP: 02140

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk

27 (B) COMPUTER: IBM PC compatible

28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

31 (vi) CURRENT APPLICATION DATA:

C--&gt; 32 (A) APPLICATION NUMBER: US/09/714,792

C--&gt; 33 (B) FILING DATE: 16-Nov-2000

34 (C) CLASSIFICATION:

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Brown, Scott A.

38 (B) REGISTRATION NUMBER: 32,724

39 (C) REFERENCE/DOCKET NUMBER: GI5268

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: (617) 498-8224

43 (B) TELEFAX: (617) 876-5851

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 1525 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: double

52 (D) TOPOLOGY: linear

54 (ii) MOLECULE TYPE: cDNA

56 (iii) HYPOTHETICAL: NO

59 (ix) FEATURE:

60 (A) NAME/KEY: CDS



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61      (B) LOCATION: 256..1404
64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
66      GAATTCGGCA CGAGGGAGAG GAGGAGGGAA AGATAGAAAAG AGAGAGAGAA AGATTGCTTG      60
68      CTACCCCTGA ACAGTGACCT CTCTCAAGAC AGTGCTTTGC TCTTCACGTA TAAGGAAGGA      120
70      AAACAGTAGA GATTCAATTT AGTGTCTAAT GTGGAAAGGA GGACAAAGAG GTCTTGTGAT      180
72      AACTGCCTGT GATAATACAT TTCTTGAGAA ACCATATTAT TGAGTAGAGC TTTCAGCACA      240
74      CTAAATCCTG GAGAA ATG GCT TTT GTG CAT ATC AGA TGC TTG TGT TTC ATT      291
75      Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile
76      1 5 10
78      CTT CTT TGT ACA ATA ACT GGC TAT TCT TTG GAG ATA AAA GTT AAT CCT      339
79      Leu Leu Cys Thr Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro
80      15 20 25
82      CCT CAG GAT TTT GAA ATA TTG GAT CCT GGA TTA CTT GGT TAT CTC TAT      387
83      Pro Gln Asp Phe Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr
84      30 35 40
86      TTG CAA TGG AAA CCT CCT GTG GTT ATA GAA AAA TTT AAG GGC TGT ACA      435
87      Leu Gln Trp Lys Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr
88      45 50 55 60
90      CTA GAA TAT GAG TTA AAA TAC CGA AAT GTT GAT AGC GAC AGC TGG AAG      483
91      Leu Glu Tyr Glu Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys
92      65 70 75
94      ACT ATA ATT ACT AGG AAT CTA ATT TAC AAG GAT GGG TTT GAT CTT AAT      531
95      Thr Ile Ile Thr Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn
96      80 85 90
98      AAA GGC ATT GAA GGA AAG ATA CGT ACG CAT TTG TCA GAG CAT TGT ACA      579
99      Lys Gly Ile Glu Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr
100     95 100 105
102     AAT GGA TCA GAA GTA CAA AGT CCA TGG ATA GAA GCT TCT TAT GGG ATA      627
103     Asn Gly Ser Glu Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile
104     110 115 120
106     TCA GAT GAA GGA AGT TTG GAA ACT AAA ATT CAG GAC ATG AAG TGT ATA      675
107     Ser Asp Glu Gly Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile
108     125 130 135 140
110     TAT TAT AAC TGG CAG TAT TTG GTC TGC TCT TGG AAA CCT GGC AAG ACA      723
111     Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr
112     145 150 155
114     GTA TAT TCT GAT ACC AAC TAT ACC ATG TTT TTC TGG TAT GAG GGC TTG      771
115     Val Tyr Ser Asp Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu
116     160 165 170
118     GAT CAT GCC TTA CAG TGT GCT GAT TAC CTC CAG CAT GAT GAA AAA AAT      819
119     Asp His Ala Leu Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn
120     175 180 185
122     GTT GGA TGC AAA CTG TCC AAC TTG GAC TCA TCA GAC TAT AAA GAT TTT      867
123     Val Gly Cys Lys Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe
124     190 195 200
126     TTT ATC TGT GTT AAT GGA TCT TCA AAG TTG GAA CCC ATC AGA TCC AGC      915
127     Phe Ile Cys Val Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser
128     205 210 215 220
130     TAT ACA GTT TTT CAA CTT CAA AAT ATA GTT AAA CCA TTG CCA CCA GAA      963

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131 Tyr Thr Val Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu
132          225          230          235
134 TTC CTT CAT ATT AGT GTG GAG AAT TCC ATT GAT ATT AGA ATG AAA TGG      1011
135 Phe Leu His Ile Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp
136          240          245          250
138 AGC ACA CCT GGA GGA CCC ATT CCA CCA AGG TGT TAC ACT TAT GAA ATT      1059
139 Ser Thr Pro Gly Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile
140          255          260          265
142 GTG ATC CGA GAA GAC GAT ATT TCC TGG GAG TCT GCC ACA GAC AAA AAC      1107
143 Val Ile Arg Glu Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn
144          270          275          280
146 GAT ATG AAG TTG AAG AGG AGA GCA AAT GAA AGT GAA GAC CTA TGC TTT      1155
147 Asp Met Lys Leu Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe
148          285          290          295          300
150 TTT GTA AGA TGT AAG GTC AAT ATA TAT TGT GCA GAT GAT GGA ATT TGG      1203
151 Phe Val Arg Cys Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp
152          305          310          315
154 AGC GAA TGG AGT GAA GAG GAA TGT TGG GAA GGT TAC ACA GGG CCA GAC      1251
155 Ser Glu Trp Ser Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp
156          320          325          330
158 TCA AAG ATT ATT TTC ATA GTA CCA GTT TGT CTT TTC TTT ATA TTC CTT      1299
159 Ser Lys Ile Ile Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu
160          335          340          345
162 TTG TTA CTT CTT TGC CTT ATT GTG GAG AAG GAA GAA CCT GAA CCC ACA      1347
163 Leu Leu Leu Leu Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr
164          350          355          360
166 TTG AGC CTC CAT GTG GAT CTG AAC AAA GAA GTG TGT GCT TAT GAA GAT      1395
167 Leu Ser Leu His Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp
168          365          370          375          380
170 ACC CTC TGT TAAACCACCA ATTTCTTGAC ATAGAGCCAG CCAGCAGGAG      1444
171 Thr Leu Cys
174 TCATATTAAA CTCAATTTCT CTTAAAATTT CGAATACATC TTCTTGAAAA TCCAAAAAAA      1504
176 AAAAAAAAAA AAAAACTCGA G      1525
179 (2) INFORMATION FOR SEQ ID NO: 2:
181 (i) SEQUENCE CHARACTERISTICS:
182 (A) LENGTH: 383 amino acids
183 (B) TYPE: amino acid
184 (D) TOPOLOGY: linear
186 (ii) MOLECULE TYPE: protein
188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
190 Met Ala Phe Val His Ile Arg Cys Leu Cys Phe Ile Leu Leu Cys Thr
191 1 5 10 15
193 Ile Thr Gly Tyr Ser Leu Glu Ile Lys Val Asn Pro Pro Gln Asp Phe
194 20 25 30
196 Glu Ile Leu Asp Pro Gly Leu Leu Gly Tyr Leu Tyr Leu Gln Trp Lys
197 35 40 45
199 Pro Pro Val Val Ile Glu Lys Phe Lys Gly Cys Thr Leu Glu Tyr Glu
200 50 55 60
202 Leu Lys Tyr Arg Asn Val Asp Ser Asp Ser Trp Lys Thr Ile Ile Thr

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Input Set : N:\jumbos\714792.txt

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203	65		70		75		80
205	Arg Asn Leu Ile Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu						
206		85		90		95	
208	Gly Lys Ile Arg Thr His Leu Ser Glu His Cys Thr Asn Gly Ser Glu						
209		100		105		110	
211	Val Gln Ser Pro Trp Ile Glu Ala Ser Tyr Gly Ile Ser Asp Glu Gly						
212		115		120		125	
214	Ser Leu Glu Thr Lys Ile Gln Asp Met Lys Cys Ile Tyr Tyr Asn Trp						
215		130		135		140	
217	Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Lys Thr Val Tyr Ser Asp						
218		145		150		155	
220	Thr Asn Tyr Thr Met Phe Phe Trp Tyr Glu Gly Leu Asp His Ala Leu						
221		165		170		175	
223	Gln Cys Ala Asp Tyr Leu Gln His Asp Glu Lys Asn Val Gly Cys Lys						
224		180		185		190	
226	Leu Ser Asn Leu Asp Ser Ser Asp Tyr Lys Asp Phe Phe Ile Cys Val						
227		195		200		205	
229	Asn Gly Ser Ser Lys Leu Glu Pro Ile Arg Ser Ser Tyr Thr Val Phe						
230		210		215		220	
232	Gln Leu Gln Asn Ile Val Lys Pro Leu Pro Pro Glu Phe Leu His Ile						
233		225		230		235	
235	Ser Val Glu Asn Ser Ile Asp Ile Arg Met Lys Trp Ser Thr Pro Gly						
236		245		250		255	
238	Gly Pro Ile Pro Pro Arg Cys Tyr Thr Tyr Glu Ile Val Ile Arg Glu						
239		260		265		270	
241	Asp Asp Ile Ser Trp Glu Ser Ala Thr Asp Lys Asn Asp Met Lys Leu						
242		275		280		285	
244	Lys Arg Arg Ala Asn Glu Ser Glu Asp Leu Cys Phe Phe Val Arg Cys						
245		290		295		300	
247	Lys Val Asn Ile Tyr Cys Ala Asp Asp Gly Ile Trp Ser Glu Trp Ser						
248		305		310		315	
250	Glu Glu Glu Cys Trp Glu Gly Tyr Thr Gly Pro Asp Ser Lys Ile Ile						
251		325		330		335	
253	Phe Ile Val Pro Val Cys Leu Phe Phe Ile Phe Leu Leu Leu Leu Leu						
254		340		345		350	
256	Cys Leu Ile Val Glu Lys Glu Glu Pro Glu Pro Thr Leu Ser Leu His						
257		355		360		365	
259	Val Asp Leu Asn Lys Glu Val Cys Ala Tyr Glu Asp Thr Leu Cys						
260		370		375		380	

262 (2) INFORMATION FOR SEQ ID NO: 3:

264 (i) SEQUENCE CHARACTERISTICS:

265 (A) LENGTH: 1369 base pairs

266 (B) TYPE: nucleic acid

267 (C) STRANDEDNESS: double

268 (D) TOPOLOGY: linear

270 (ii) MOLECULE TYPE: cDNA

272 (iii) HYPOTHETICAL: NO

275 (ix) FEATURE:

276 (A) NAME/KEY: CDS



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277      (B) LOCATION: 103..1245
280      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
282      GGATCCGCGC GGATGAAGGC TATTTGAAGT CGCCATAACC TGGTCAGAAG TGTGCCTGTC      60
284      GGC GGGGAGA GAGGCAATAT CAAGGTTTTA AATCTCGGAG AA ATG GCT TTC GTT      114
285                                     Met Ala Phe Val
286                                     1
288      TGC TTG GCT ATC GGA TGC TTA TAT ACC TTT CTG ATA AGC ACA ACA TTT      162
289      Cys Leu Ala Ile Gly Cys Leu Tyr Thr Phe Leu Ile Ser Thr Thr Phe
290      5 10 15 20
292      GGC TGT ACT TCA TCT TCA GAC ACC GAG ATA AAA GTT AAC CCT CCT CAG      210
293      Gly Cys Thr Ser Ser Ser Asp Thr Glu Ile Lys Val Asn Pro Pro Gln
294      25 30 35
296      GAT TTT GAG ATA GTG GAT CCC GGA TAC TTA GGT TAT CTC TAT TTG CAA      258
297      Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln
298      40 45 50
300      TGG CAA CCC CCA CTG TCT CTG GAT CAT TTT AAG GAA TGC ACA GTG GAA      306
301      Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu Cys Thr Val Glu
302      55 60 65
304      TAT GAA CTA AAA TAC CGA AAC ATT GGT AGT GAA ACA TGG AAG ACC ATC      354
305      Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile
306      70 75 80
308      ATT ACT AAG AAT CTA CAT TAC AAA GAT GGG TTT GAT CTT AAC AAG GGC      402
309      Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly
310      85 90 95 100
312      ATT GAA GCG AAG ATA CAC ACG CTT TTA CCA TGG CAA TGC ACA AAT GGA      450
313      Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly
314      105 110 115
316      TCA GAA GTT CAA AGT TCC TGG GCA GAA ACT ACT TAT TGG ATA TCA CCA      498
317      Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro
318      120 125 130
320      CAA GGA ATT CCA GAA ACT AAA GTT CAG GAT ATG GAT TGC GTA TAT TAC      546
321      Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp Cys Val Tyr Tyr
322      135 140 145
324      AAT TGG CAA TAT TTA CTC TGT TCT TGG AAA CCT GGC ATA GGT GTA CTT      594
325      Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly Ile Gly Val Leu
326      150 155 160
328      CTT GAT ACC AAT TAC AAC TTG TTT TAC TGG TAT GAG GGC TTG GAT CAT      642
329      Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His
330      165 170 175 180
332      GCA TTA CAG TGT GTT GAT TAC ATC AAG GCT GAT GGA CAA AAT ATA GGA      690
333      Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly
334      185 190 195
336      TGC AGA TTT CCC TAT TTG GAG GCA TCA GAC TAT AAA GAT TTC TAT ATT      738
337      Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile
338      200 205 210
340      TGT GTT AAT GGA TCA TCA GAG AAC AAG CCT ATC AGA TCC AGT TAT TTC      786
341      Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe
342      215 220 225
344      ACT TTT CAG CTT CAA AAT ATA GTT AAA CCT TTG CCG CCA GTC TAT CTT      834

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/714,792

DATE: 04/10/2002

TIME: 18:20:45

Input Set : N:\jumbos\714792.txt

Output Set: N:\CRF3\04102002\I714792.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:480 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5  
L:495 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6  
L:510 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7  
L:525 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8  
L:540 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9